

Amendments to the Claims

Please cancel Claim 6. Please amend Claims 1-5 and 7-12 as indicated below. The Claim Listing below will replace all prior versions of the claims in the application:

Claim Listing

1. (Currently amended) A An *in vitro* method of defining the differentiation grade of a tumor with genes and/or proteins selected by the statistical analyses based on the expression level or pattern levels or patterns of the genes and/or proteins of human tumor tissues obtainable obtained from cancer patients, wherein the genes and/or proteins are selected in descending order of Fisher ratio and wherein the expression levels or patterns of genes and/or proteins are determined by performing an assay for the gene and/or protein levels and patterns.
2. (Currently amended) A The *in vitro* method according to claim 1, wherein the human tissues are human liver tissues.
3. (Currently amended) A The *in vitro* method according to claim 2, wherein the differentiation grade of a tumor is selected from the group consisting of non-cancerous liver, pre-cancerous liver, well differentiated hepatocellular carcinoma (HCC), moderately differentiated HCC, and poorly differentiated HCC.
4. (Currently amended) A The *in vitro* method according to claim 3, wherein the genes and/or proteins are differentially expressed between non-cancerous liver and pre-cancerous liver, pre-cancerous liver and well differentiated hepatocellular carcinoma (HCC), well differentiated HCC and moderately differentiated HCC, or moderately differentiated HCC and poorly differentiated HCC.
5. (Currently amended) A The *in vitro* method according to claim 4, wherein the assay is selected from the group consisting of the expression level or pattern of genes and/or proteins is examined by means of DNA microarray, reverse transcription polymerase-

chain reaction, northern blotting, *in situ* hybridization, ribonuclease protection assay, western blot, enzyme-linked immunosorbent assay or and protein array.

6. (Canceled)
7. (Currently amended) A The *in vitro* method according to claim 6 1, wherein the selected genes and/or proteins are in a number that the number of the genes and/or proteins is between 40 and 100.
8. (Currently amended) A The *in vitro* method according to claim 6 1, wherein the selected genes and/or proteins are in a number that the number of the genes and/or proteins is between 35 and 45.
9. (Currently amended) A The *in vitro* method according to claim 8, wherein the number of the genes and/or proteins is 40.
10. (Currently amended) A An *in vitro* method of defining the differentiation grade of a hepatocellular carcinoma (HCC) tumor, the method comprising the steps of:
 - (a) determining expression levels or patterns of genes and/or proteins in human liver tissues selected from the group consisting of non-cancerous liver, pre-cancerous liver, well differentiated HCC tumor, moderately differentiated HCC tumor and poorly differentiated HCC tumor; and
 - (b) selecting genes and/or proteins that have the highest Fisher ratios in comparison between said non-cancerous liver and said pre-cancerous liver, said pre-cancerous liver and said well differentiated HCC tumor, said well differentiated HCC tumor and said moderately differentiated HCC tumor, or said moderately differentiated HCC tumor and said poorly differentiated HCC tumor[[;]] and
 - (b) thereby defining the differentiation grade of a tumor by using the genes and/or proteins.

11. (Currently amended) A An *in vitro* method of defining the differentiation grade of a hepatocellular carcinoma (HCC) tumor, the method comprising the steps of:

(a) determining expression levels or patterns of genes and/or proteins in human liver tissues selected from the group consisting of non-cancerous liver, pre-cancerous liver, well differentiated hepatocellular carcinoma (HCC) tumor, moderately differentiated HCC tumor and poorly differentiated HCC tumor;

(b) determining the a number of genes and/or proteins to define the differentiation grade of a tumor; and

(b)(c) selecting a number of genes and/or proteins in descending order of Fisher ratio in the number determined decided in step (a) (b) that have, wherein the highest Fisher ratios ratio is applied in comparison of said gene and/or protein expression levels or patterns determined in step (a) between non-cancerous liver and pre-cancerous liver, pre-cancerous liver and well differentiated hepatocellular carcinoma (HCC), well differentiated HCC and moderately differentiated HCC, or moderately differentiated HCC and poorly differentiated HCC[[:]];

(e) applying the data of genes and/or proteins selected in step (b) to all samples; and

(d) thereby defining the differentiation grade of a HCC tumor.

12. (Currently amended) A An *in vitro* method of defining the differentiation grade of a hepatocellular carcinoma (HCC) tumor, the method comprising the steps of:

(a) determining expression levels or patterns of genes and/or proteins in human liver tissues selected from the group consisting of non-cancerous liver, pre-cancerous liver, well differentiated hepatocellular carcinoma (HCC) tumor, moderately differentiated HCC tumor and poorly differentiated HCC tumor;

(b) determining the a number of genes and/or proteins to define the differentiation grade of a tumor;

(b)(c) selecting a number of genes and/or proteins in descending order of Fisher ratio in the number determined decided in step (a) (b) that have, wherein the highest Fisher ratios criterion is applied in comparison of said gene and/or protein expression levels or patterns determined in step (a) between non-cancerous liver

and pre-cancerous liver, pre-cancerous liver and well differentiated hepatocellular carcinoma (HCC), well differentiated HCC and moderately differentiated HCC, or moderately differentiated HCC and poorly differentiated HCC;

- (e) applying the data of genes and/or proteins selected in step (b) to all samples;
- (d) designing a minimum distance classifier with the expression data of the genes and/or proteins selected in step (b) (c);
- (e) applying the minimum distance classifier designed in step (d) to all samples the genes and/or proteins selected in step (c);
- (f) generating self-organizing map with the expression data of all the genes and/or proteins selected in step (b) (c); and
- (g) applying the self organizing map generated in step (f), to all samples; and
- (h) thereby defining the differentiation grade of a tumor.

13. (Withdrawn) A kit for carrying out the method according to claim 1, the kit comprises DNA chips, oligonucleotide chips, protein chips, probes or primers that are necessary for effecting DNA microarrays, oligonucleotide microarrays, protein arrays, northern blotting, RNase protection assays, western blotting, and reverse transcription polymerase-chain reaction to examine the expression of the genes and/or proteins selected by the statistical analyses in claim 1.

14. (Withdrawn) Use of genes and/or proteins according to any one of claim 1 for screening anti-cancer agents.

15. (Withdrawn) Use of antibodies specific to genes and/or proteins according to claim 1 for treating tumors in different grades.